REMARKS

Claims 1-12 and 15 are pending in the present Application. Claims 3 and 8 have been canceled, claims 1, 7, and 12 have been amended; leaving claims 1-2, 4-7, 9-12, and 15 for consideration upon entry of the present Amendment.

Reconsideration and allowance of the claims are respectfully requested in view of the above amendments and the following remarks.

Claim Amendments

Claim 1 is amended to incorporate the limitations of cancelled claim 3.

Claims 7 and 12 are amended to incorporate the limitations of cancelled claim 8.

Claim Rejections Under 35 U.S.C. § 103(a)

Claims 1-12 and 15 stand rejected under 35 U.S.C. § 103(a), as being unpatentable over Benson et al. (Nucleic Acids Research, 1999, Vol. 27, pages 38-43) (previously cited; hereinafter "Benson"). Applicants respectfully traverse this rejection.

For an obviousness rejection to be proper, the Examiner must meet the burden of establishing that all elements of the invention are disclosed in the prior art. *In re Fine*, 5 U.S.P.Q.2d 1596, 1598 (Fed. Cir. 1988). "A patent composed of several elements is not proved obvious merely by demonstrating that each of its elements was, independently, known in the prior art." *KSR Int'l Co. v. Teleflex Inc.,* 127 S.Ct. 1727, 1741 (2007). To find obviousness, the Examiner must "identify a reason that would have prompted a person of ordinary skill in the art in the relevant field to combine the elements in the way the claimed new invention does." *Id*.

The claimed invention is drawn to a system and method for determining a location of a target sequence in a genome sequence, and to a computer readable medium having embodied thereon a computer program comprising computer readable code for executing the method.

Claim 1 is drawn to a system for determining a location of a target sequence in a genome sequence, comprising: a storage unit for storing a crosslink map, wherein the crosslink map comprises records of sequence information for a plurality of versions of a genome sequence; an information search unit, for searching for identifier information and sequence information corresponding to a target sequence among the records in the crosslink map; and a location

estimation unit, for determining a reference group comprising a reference sequence information for an organism, wherein the reference sequence information is represented in the crosslink map by more than a predetermined number of records; calculating a difference value of a start position and an end position of the reference sequence information obtained from the crosslink map; and determining a location of the target sequence in the genome sequence by a location shift corresponding to the difference value, wherein a record for a sequence information in the crosslink map comprises a name of a genome sequence, a version of the genome sequence, an identifier of a sequence information in the genome sequence, a start position and an end position of the sequence information in the genome sequence, and a length of the sequence information in the genome sequence.

Claim 7 is drawn to a method of determining a location of a target sequence in a genome sequence, the method comprising: inputting a target sequence; searching for identifier information and sequence information corresponding to the target sequence in a crosslink map, wherein the crosslink map comprises records of sequence information for a plurality of versions of a genome sequence; determining a reference group comprising a reference sequence information for an organism, wherein the reference sequence information is represented in the crosslink map by more than a predetermined number of records; calculating a difference value of a start position and an end position of the reference sequence information obtained from the crosslink map; determining a location of the target sequence in the genome sequence by a location shift corresponding to the difference value; and outputting the location of the target sequence in the genome sequence to a user, wherein a record for a sequence information recorded in the crosslink map comprises a name of a genome sequence, a version of the genome sequence, an identifier for a sequence information in the genome sequence, a start position and an end position of the sequence information in the genome sequence, and a length of the sequence information in the genome sequence.

Claim 12 is drawn to a computer readable medium having embodied thereon a computer program comprising computer readable code for executing the method of claim 7.

Benson et al. provide a general description of certain aspects of the GenBank® public database of nucleotide and protein sequences. (p. 12, 1st col., Introduction) Benson et al. describe the organization of GenBank (pp. 38-40); how the database is built by input of new

sequences via one of two programs, Bankit or Sequin (pp. 40-41); and retrieving GenBank data using Entrez (pp. 41-42), performing sequence similarity searching with the BLAST family of search programs (p. 42), or accessing GenBank via other means, such as anonymous FTP (p. 42). Benson discloses general facts about the function of some members of the BLAST family of search programs. For example, Benson discloses that a BLAST 2.0 search accepts a query sequence and the similarity search is performed using a PAM or BLOSUM scoring matrix, resulting in a set of gapped alignments. (p. 42, 2nd full para.)

However, Benson et al. are silent with respect to at least a location estimation unit, for determining a reference group comprising a reference sequence information for an organism, wherein the reference sequence information is represented in the crosslink map by more than a predetermined number of records; calculating a difference value of a start position and an end position of the reference sequence information obtained from the crosslink map; and determining a location of the target sequence in the genome sequence by a location shift corresponding to the difference value, while Benson only discloses BLAST for searching the database for a query sequence as recited in claim 1, or the elements determining a reference group comprising a reference sequence information for an organism, wherein the reference sequence information is represented in the crosslink map by more than a predetermined number of records; calculating a difference value of a start position and an end position of the reference sequence information obtained from the crosslink map; and determining a location of the target sequence in the genome sequence by a location shift corresponding to the difference value recited in claims 7 and 12.

The Office Action states on p. 4, 1st full para. that Benson et al. do not explicitly disclose a location estimation unit as recited in claim 1 and then alleges that "given that all the functions performed by these units in the claims are also performed in Benson et al., it would have been obvious to one of ordinary skill in the art that the system of BLAST + GENBANK" includes such a unit. However, the Office Action fails to provide any evidence documenting that Benson does in fact disclose a unit performing the functions of the location estimation unit as recited in claim 1 or that Benson discloses the following elements of claims 7 and 12: determining a reference group comprising a reference sequence information for an organism, wherein the reference sequence information is represented in the crosslink map by more than a predetermined number of records; calculating a difference value of a start position and an end position of the reference sequence

information obtained from the crosslink map; and determining a location of the target sequence in the genome sequence by a location shift corresponding to the difference value.

Applicants maintain that the Examiner has used an improper standard in arriving at the rejection of the above claims under section 103, based on improper hindsight given the guidance of the instant specification and claims, which fails to consider the totality of applicant's invention and the totality of the cited reference. Section 103 sets out the test for obviousness determinations. It states, in pertinent part, that such determinations are to be made by consideration of

> . . . the differences between subject matter sought to be patented and the prior art such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the [pertinent] art.

In making a Section 103 rejection, the Examiner bears the burden of establishing a prima facie case of obviousness. In re Fine, 5 U.S.P.Q. 2d 1596, 1598 (Fed. Cir. 1998). The Examiner ". . . can satisfy this burden only by showing some objective teaching in the prior art or that knowledge generally available to one of ordinary skill in art would lead that individual to combine the relevant teachings of the references". Id Applicants assert that the Examiner has failed to provide the required showing that Benson teaches these elements or that the knowledge was generally available to one of ordinary skill in the art.

Further, while the Office Action states that BLAST uses a query sequence to search the entire database to find homologous sequences and locations of the query sequence in the sequences in the database, it does not cite anywhere in Benson et al. that the following limitations of claim 7 are taught: determining a reference group comprising a reference sequence information for an organism, wherein the reference sequence information is represented in the crosslink map by more than a predetermined number of records; calculating a difference value of a start position and an end position of the reference sequence information obtained from the crosslink map; or determining a location of the target sequence in the genome sequence by a location shift corresponding to the difference value. Neither does the Office Action explain what general knowledge of one of skill in the art at the time the claimed invention was made supplements the teachings of Benson et al. that would render the method of claims 7 and 9-11 obvious. Thus, Applicants assert that the Office Action has failed to establish that claims 7 and 9-11 are obvious over Benson et al.

Furthermore, as Benson et al. fails to teach all limitations of the method of claim 7 and 10-11 as noted above, Benson et al. cannot teach all elements of the computer readable medium of claim 12 having embodied thereon a computer program comprising computer readable code for executing the method of claim 7, nor can Benson et al. teach all the functional limitations for components of the system of claims 1-2, 4-6 and 15 for performing the method for determining a location of a target sequence in a genome sequence. Therefore Applicants assert that the Office Action also fails to establish that claims 1-2, 4-6, 12, and 15 are obvious over Benson et al.

Applicants request reconsideration and withdrawal of the rejection of claims 1-2, 4-7, 9-12 and 15 under 35 U.S.C. § 103(a), as being obvious over Benson et al.

It is believed that the foregoing amendments and remarks fully comply with the Office Action and that the claims herein should now be allowable to Applicants. Accordingly, reconsideration and allowance are requested.

If there are any additional charges with respect to this Amendment or otherwise, please charge them to Deposit Account No. 06-1130.

Respectfully submitted,

CANTOR COLBURN LLP

/Sandra L. Shaner/
By_____
Sandra L. Shaner, PhD
Registration No. 47,934

Date: January 11, 2009
CANTOR COLBURN LLP
20 Church Street, 22nd Floor
Hartford, CT 06130-3207
Telephone (860) 286-2929
Facsimile (860) 286-0115
Customer No.: 23413